

5630 QB #6



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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/830,751

DATE: 01/24/2003

TIME: 13:11:20

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Output Set: N:\CRF4\01242003\I830751.raw

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3 <110> APPLICANT: Suthers, Patrick F
4   Cameron, Douglas C.
6 <120> TITLE OF INVENTION: Production of 3-Hydroxypropionic Acid in Recombinant
7   Organisms
9 <130> FILE REFERENCE: 960296.96617
11 <140> CURRENT APPLICATION NUMBER: 09/830,751
12 <141> CURRENT FILING DATE: 2000-08-30
14 <150> PRIOR APPLICATION NUMBER: 60/151,440
15 <151> PRIOR FILING DATE: 1999-08-30
17 <150> PRIOR APPLICATION NUMBER: PCT/US00/23878
18 <151> PRIOR FILING DATE: 2000-08-30
20 <160> NUMBER OF SEQ ID NOS: 23
22 <170> SOFTWARE: PatentIn Ver. 2.1
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 1529
26 <212> TYPE: DNA
27 <213> ORGANISM: Saccharomyces cerevisiae
29 <220> FEATURE:
30 <221> NAME/KEY: CDS
31 <222> LOCATION: (25)..(1509)
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36                               1           5
38 atc aag ctg ccc aat ggg ttg gaa tat gag caa cca acg ggg ttg ttc      99
39 Ile Lys Leu Pro Asn Gly Leu Glu Tyr Glu Gln Pro Thr Gly Leu Phe
40 10           15           20           25
42 atc aac aac aag ttt gtt cct tct aaa cag aac aag acc ttc gaa gtc      147
43 Ile Asn Asn Lys Phe Val Pro Ser Lys Gln Asn Lys Thr Phe Glu Val
44           30           35           40
46 att aac cct tcc acg gaa gaa gaa ata tgt cat att tat gaa ggt aga      195
47 Ile Asn Pro Ser Thr Glu Glu Glu Ile Cys His Ile Tyr Glu Gly Arg
48           45           50           55
50 gag gac gat gtg gaa gag gcc gtg cag gcc gcc gac cgt gcc ttc tct      243
51 Glu Asp Asp Val Glu Glu Ala Val Gln Ala Ala Asp Arg Ala Phe Ser
52           60           65           70
54 aat ggg tct tgg aac ggt atc gac cct att gac agg ggt aag gct ttg      291
55 Asn Gly Ser Trp Asn Gly Ile Asp Pro Ile Asp Arg Gly Lys Ala Leu
56           75           80           85
58 tac agg tta gcc gaa tta att gaa cag gac aag gat gtc att gct tcc      339
59 Tyr Arg Leu Ala Glu Leu Ile Glu Gln Asp Lys Asp Val Ile Ala Ser
60 90           95           100           105
62 atc gag act ttg gat aac ggt aaa gct atc tct tcc tcg aga gga gat      387

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63	Ile	Glu	Thr	Leu	Asp	Asn	Gly	Lys	Ala	Ile	Ser	Ser	Ser	Arg	Gly	Asp	
64					110					115					120		
66	gtt	gat	tta	gtc	atc	aac	tat	ttg	aaa	tct	tct	gct	ggc	ttt	gct	gat	435
67	Val	Asp	Leu	Val	Ile	Asn	Tyr	Leu	Lys	Ser	Ser	Ala	Gly	Phe	Ala	Asp	
68				125					130					135			
70	aaa	att	gat	ggg	aga	atg	att	gat	act	ggg	aga	acc	cat	ttt	tct	tac	483
71	Lys	Ile	Asp	Gly	Arg	Met	Ile	Asp	Thr	Gly	Arg	Thr	His	Phe	Ser	Tyr	
72			140					145					150				
74	act	aag	aga	cag	cct	ttg	ggg	gtt	tgt	ggg	cag	att	att	cct	tgg	aat	531
75	Thr	Lys	Arg	Gln	Pro	Leu	Gly	Val	Cys	Gly	Gln	Ile	Ile	Pro	Trp	Asn	
76		155					160					165					
78	ttc	cca	ctg	ttg	atg	tgg	gcc	tgg	aag	att	gcc	cct	gct	ttg	gtc	acc	579
79	Phe	Pro	Leu	Leu	Met	Trp	Ala	Trp	Lys	Ile	Ala	Pro	Ala	Leu	Val	Thr	
80	170					175					180				185		
82	ggg	aac	acc	gtc	gtg	ttg	aag	act	gcc	gaa	tcc	acc	cca	ttg	tcc	gct	627
83	Gly	Asn	Thr	Val	Val	Leu	Lys	Thr	Ala	Glu	Ser	Thr	Pro	Leu	Ser	Ala	
84				190						195				200			
86	ttg	tat	gtg	tct	aaa	tac	atc	cca	cag	gcg	ggg	att	cca	cct	ggg	gtg	675
87	Leu	Tyr	Val	Ser	Lys	Tyr	Ile	Pro	Gln	Ala	Gly	Ile	Pro	Pro	Gly	Val	
88			205					210					215				
90	atc	aac	att	gta	tcc	ggg	ttt	ggg	aag	att	gtg	gtt	gag	gcc	att	aca	723
91	Ile	Asn	Ile	Val	Ser	Gly	Phe	Gly	Lys	Ile	Val	Val	Glu	Ala	Ile	Thr	
92		220					225						230				
94	aac	cat	cca	aaa	atc	aaa	aag	gtt	gcc	ttc	aca	ggg	tcc	acg	gct	acg	771
95	Asn	His	Pro	Lys	Ile	Lys	Lys	Val	Ala	Phe	Thr	Gly	Ser	Thr	Ala	Thr	
96		235				240					245						
98	ggg	aga	cac	att	tac	cag	tcc	gca	gcc	gca	ggc	ttg	aaa	aaa	gtg	act	819
99	Gly	Arg	His	Ile	Tyr	Gln	Ser	Ala	Ala	Ala	Gly	Leu	Lys	Lys	Val	Thr	
100	250					255					260				265		
102	ttg	gag	ctg	ggg	ggg	aaa	tca	cca	aac	att	gtc	ttc	gcg	gac	gcc	gag	867
103	Leu	Glu	Leu	Gly	Gly	Lys	Ser	Pro	Asn	Ile	Val	Phe	Ala	Asp	Ala	Glu	
104				270						275				280			
106	ttg	aaa	aaa	gcc	gtg	caa	aac	att	atc	ctt	ggg	atc	tac	tac	aat	tct	915
107	Leu	Lys	Lys	Ala	Val	Gln	Asn	Ile	Ile	Leu	Gly	Ile	Tyr	Tyr	Asn	Ser	
108			285					290					295				
110	ggg	gag	gtc	tgt	tgt	gcg	ggg	tca	agg	gtg	tat	gtt	gaa	gaa	tct	att	963
111	Gly	Glu	Val	Cys	Cys	Ala	Gly	Ser	Arg	Val	Tyr	Val	Glu	Glu	Ser	Ile	
112		300					305						310				
114	tac	gac	aaa	ttc	att	gaa	gag	ttc	aaa	gcc	gct	tct	gaa	tcc	atc	aag	1011
115	Tyr	Asp	Lys	Phe	Ile	Glu	Glu	Phe	Lys	Ala	Ala	Ser	Glu	Ser	Ile	Lys	
116		315				320					325						
118	gtg	ggc	gac	cca	ttc	gat	gaa	tct	act	ttc	caa	ggg	gca	caa	acc	tct	1059
119	Val	Gly	Asp	Pro	Phe	Asp	Glu	Ser	Thr	Phe	Gln	Gly	Ala	Gln	Thr	Ser	
120	330					335					340				345		
122	caa	atg	caa	cta	aac	aaa	atc	ttg	aaa	tac	gtt	gac	att	ggg	aag	aat	1107
123	Gln	Met	Gln	Leu	Asn	Lys	Ile	Leu	Lys	Tyr	Val	Asp	Ile	Gly	Lys	Asn	
124				350				355					360				
126	gaa	ggg	gct	act	ttg	att	acc	ggg	ggg	gaa	aga	tta	ggg	agc	aag	ggg	1155
127	Glu	Gly	Ala	Thr	Leu	Ile	Thr	Gly	Gly	Glu	Arg	Leu	Gly	Ser	Lys	Gly	

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128          365          370          375
130 tac ttc att aag cca act gtc ttt ggt gac gtt aag gaa gac atg aga 1203
131 Tyr Phe Ile Lys Pro Thr Val Phe Gly Asp Val Lys Glu Asp Met Arg
132          380          385          390
134 att gtc aaa gag gaa atc ttt ggc cct gtt gtc act gta acc aaa ttc 1251
135 Ile Val Lys Glu Glu Ile Phe Gly Pro Val Val Thr Val Thr Lys Phe
136          395          400          405
138 aaa tct gcc gac gaa gtc att aac atg gcg aac gat tct gaa tac ggg 1299
139 Lys Ser Ala Asp Glu Val Ile Asn Met Ala Asn Asp Ser Glu Tyr Gly
140 410          415          420          425
142 ttg gct gct ggt att cac acc tct aat att aat acc gcc tta aaa gtg 1347
143 Leu Ala Ala Gly Ile His Thr Ser Asn Ile Asn Thr Ala Leu Lys Val
144          430          435          440
146 gct gat aga gtt aat gcg ggt acg gtc tgg ata aac act tat aac gat 1395
147 Ala Asp Arg Val Asn Ala Gly Thr Val Trp Ile Asn Thr Tyr Asn Asp
148          445          450          455
150 ttc cac cac gca gtt cct ttc ggt ggg ttc aat gca tct ggt ttg ggc 1443
151 Phe His His Ala Val Pro Phe Gly Gly Phe Asn Ala Ser Gly Leu Gly
152          460          465          470
154 agg gaa atg tct gtt gat gct tta caa aac tac ttg caa gtt aaa gcg 1491
155 Arg Glu Met Ser Val Asp Ala Leu Gln Asn Tyr Leu Gln Val Lys Ala
156          475          480          485
158 gtc cgt gcc aaa ttg gac gagtaagagc tcgaattcgc 1529
159 Val Arg Ala Lys Leu Asp
160 490          495
163 <210> SEQ ID NO: 2
164 <211> LENGTH: 495
165 <212> TYPE: PRT
166 <213> ORGANISM: Saccharomyces cerevisiae
168 <400> SEQUENCE: 2
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172 Glu Tyr Glu Gln Pro Thr Gly Leu Phe Ile Asn Asn Lys Phe Val Pro
173          20          25          30
175 Ser Lys Gln Asn Lys Thr Phe Glu Val Ile Asn Pro Ser Thr Glu Glu
176          35          40          45
178 Glu Ile Cys His Ile Tyr Glu Gly Arg Glu Asp Asp Val Glu Glu Ala
179          50          55          60
181 Val Gln Ala Ala Asp Arg Ala Phe Ser Asn Gly Ser Trp Asn Gly Ile
182 65          70          75          80
184 Asp Pro Ile Asp Arg Gly Lys Ala Leu Tyr Arg Leu Ala Glu Leu Ile
185          85          90          95
187 Glu Gln Asp Lys Asp Val Ile Ala Ser Ile Glu Thr Leu Asp Asn Gly
188          100          105          110
190 Lys Ala Ile Ser Ser Ser Arg Gly Asp Val Asp Leu Val Ile Asn Tyr
191          115          120          125
193 Leu Lys Ser Ser Ala Gly Phe Ala Asp Lys Ile Asp Gly Arg Met Ile
194          130          135          140
196 Asp Thr Gly Arg Thr His Phe Ser Tyr Thr Lys Arg Gln Pro Leu Gly

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197 145          150          155          160
199 Val Cys Gly Gln Ile Ile Pro Trp Asn Phe Pro Leu Leu Met Trp Ala
200          165          170          175
202 Trp Lys Ile Ala Pro Ala Leu Val Thr Gly Asn Thr Val Val Leu Lys
203          180          185          190
205 Thr Ala Glu Ser Thr Pro Leu Ser Ala Leu Tyr Val Ser Lys Tyr Ile
206          195          200          205
208 Pro Gln Ala Gly Ile Pro Pro Gly Val Ile Asn Ile Val Ser Gly Phe
209          210          215          220
211 Gly Lys Ile Val Val Glu Ala Ile Thr Asn His Pro Lys Ile Lys Lys
212 225          230          235          240
214 Val Ala Phe Thr Gly Ser Thr Ala Thr Gly Arg His Ile Tyr Gln Ser
215          245          250          255
217 Ala Ala Ala Gly Leu Lys Lys Val Thr Leu Glu Leu Gly Gly Lys Ser
218          260          265          270
220 Pro Asn Ile Val Phe Ala Asp Ala Glu Leu Lys Lys Ala Val Gln Asn
221          275          280          285
223 Ile Ile Leu Gly Ile Tyr Tyr Asn Ser Gly Glu Val Cys Cys Ala Gly
224          290          295          300
226 Ser Arg Val Tyr Val Glu Glu Ser Ile Tyr Asp Lys Phe Ile Glu Glu
227 305          310          315          320
229 Phe Lys Ala Ala Ser Glu Ser Ile Lys Val Gly Asp Pro Phe Asp Glu
230          325          330          335
232 Ser Thr Phe Gln Gly Ala Gln Thr Ser Gln Met Gln Leu Asn Lys Ile
233          340          345          350
235 Leu Lys Tyr Val Asp Ile Gly Lys Asn Glu Gly Ala Thr Leu Ile Thr
236          355          360          365
238 Gly Gly Glu Arg Leu Gly Ser Lys Gly Tyr Phe Ile Lys Pro Thr Val
239          370          375          380
241 Phe Gly Asp Val Lys Glu Asp Met Arg Ile Val Lys Glu Glu Ile Phe
242 385          390          395          400
244 Gly Pro Val Val Thr Val Thr Lys Phe Lys Ser Ala Asp Glu Val Ile
245          405          410          415
247 Asn Met Ala Asn Asp Ser Glu Tyr Gly Leu Ala Ala Gly Ile His Thr
248          420          425          430
250 Ser Asn Ile Asn Thr Ala Leu Lys Val Ala Asp Arg Val Asn Ala Gly
251          435          440          445
253 Thr Val Trp Ile Asn Thr Tyr Asn Asp Phe His His Ala Val Pro Phe
254          450          455          460
256 Gly Gly Phe Asn Ala Ser Gly Leu Gly Arg Glu Met Ser Val Asp Ala
257 465          470          475          480
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260          485          490          495

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264 <210> SEQ ID NO: 3

265 <211> LENGTH: 1541

266 <212> TYPE: DNA

267 <213> ORGANISM: Homo sapiens

269 <220> FEATURE:

270 <221> NAME/KEY: CDS

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271 <222> LOCATION: (22)..(1521)

273 <400> SEQUENCE: 3

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279 Ala Pro Asn Gln Gln Pro Glu Val Phe Cys Asn Gln Ile Phe Ile Asn
280                               15                               20                               25
282 aat gaa tgg cac gat gcc gtc agc agg aaa aca ttc ccc acc gtc aat 147
283 Asn Glu Trp His Asp Ala Val Ser Arg Lys Thr Phe Pro Thr Val Asn
284                               30                               35                               40
286 ccg tcc act gga gag gtc atc tgt cag gta gct gaa ggg gac aag gaa 195
287 Pro Ser Thr Gly Glu Val Ile Cys Gln Val Ala Glu Gly Asp Lys Glu
288                               45                               50                               55
290 gat gtg gac aag gca cgt gaa ggc cgc ccg ggc gcc ttc cag ctg ggc 243
291 Asp Val Asp Lys Ala Arg Glu Gly Arg Pro Gly Ala Phe Gln Leu Gly
292                               60                               65                               70
294 tca cct tgg cgc cgc atg gac gca tca cac agc ggc cgg ctg ctg aac 291
295 Ser Pro Trp Arg Arg Met Asp Ala Ser His Ser Gly Arg Leu Leu Asn
296                               75                               80                               85                               90
298 cgc ctg gcc gat ctg atc gag cgg gac cgg acc tac ctg gcg gcc ttg 339
299 Arg Leu Ala Asp Leu Ile Glu Arg Asp Arg Thr Tyr Leu Ala Ala Leu
300                               95                               100                               105
302 gag acc ctg gac aat ggc aag ccc tat gtc atc tcc tac ctg gtg gat 387
303 Glu Thr Leu Asp Asn Gly Lys Pro Tyr Val Ile Ser Tyr Leu Val Asp
304                               110                               115                               120
306 ttg gac atg gtc ctc aaa tgt ctc cgg tat tat gcc ggc tgg gct gat 435
307 Leu Asp Met Val Leu Lys Cys Leu Arg Tyr Tyr Ala Gly Trp Ala Asp
308                               125                               130                               135
310 aag tac cac ggg aaa acc atc ccc att gac gga gac ttc ttc agc tac 483
311 Lys Tyr His Gly Lys Thr Ile Pro Ile Asp Gly Asp Phe Phe Ser Tyr
312                               140                               145                               150
314 aca cgc cat gaa cct gtg ggg gtg tgc ggg cag atc att ccg tgg aat 531
315 Thr Arg His Glu Pro Val Gly Val Cys Gly Gln Ile Ile Pro Trp Asn
316                               155                               160                               165                               170
318 ttc ccg ctc ctg atg caa gca tgg aag ctg ggc cca gcc ttg gca act 579
319 Phe Pro Leu Leu Met Gln Ala Trp Lys Leu Gly Pro Ala Leu Ala Thr
320                               175                               180                               185
322 gga aac gtg gtt gtg atg aag gta gct gag cag aca ccc ctc acc gcc 627
323 Gly Asn Val Val Val Met Lys Val Ala Glu Gln Thr Pro Leu Thr Ala
324                               190                               195                               200
326 ctc tat gtg gcc aac ctg atc aag gag gct ggc ttt ccc cct ggt gtg 675
327 Leu Tyr Val Ala Asn Leu Ile Lys Glu Ala Gly Phe Pro Pro Gly Val
328                               205                               210                               215
330 gtc aac att gtg cct gga ttt ggc ccc acg gct ggg gcc gcc att gcc 723
331 Val Asn Ile Val Pro Gly Phe Gly Pro Thr Ala Gly Ala Ala Ile Ala
332                               220                               225                               230
334 tcc cat gag gat gtg gac aaa gtg gca ttc aca ggc tcc act gag att 771
335 Ser His Glu Asp Val Asp Lys Val Ala Phe Thr Gly Ser Thr Glu Ile

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